GenCore version 5.1.8
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OM protein - nucleic search, using frame_plus_p2n model

Run on: May 21, 2006, 20:02:43 ; Search time 8033 Seconds
                                           (without alignments)
                                           7140.649 Million cell updates/sec

Title: US-10-673-935-2
Perfect score: 3244
Sequence: 1 MESALYPIQNKYRFNTLMNG..........RDREPKDIAFTLKKRWQQLN 598

Scoring table: BLOSUM62
                 Xgapop 10.0 , Xgapext 0.5
                 Ygapop 10.0 , Ygapext 0.5
                 Fgapop 6.0 , Fgapext 7.0
                 Delop   6.0 , Delext   7.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp
-Q=/abss/ABSSWEB_spool/US10673935/runat_19052006_150450_516/app_query.fasta_1
-DB=GenEmbl -QFMT=fastap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss06p
-USER=US10673935_@CGN_1_1_8328_@runat_19052006_150450_516 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :   GenEmbl:*
                 1: gb_env:*
                 2: gb_pat:*
                 3: gb_ph:*
                 4: gb_pl:*
                 5: gb_pr:*
                 6: gb_ro:*
                 7: gb_sts:*
                 8: gb_sy:*
                 9: gb_un:*
                 10: gb_vi:*
                 11: gb_ov:*
                 12: gb_htg:*
                 13: gb_in:*
                 14: gb_om:*
                 15: gb_ba:*

       Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	3244	100.0	2150	2	AR438771	AR438771 Sequence
	2	3244	100.0	5438	15	AF305888	AF305888 Lactobaci
	3	1779	54.8	4537	15	AY307023	AY307023 Ruminococ
c	4	1270	39.1	3448	15	CPE420784	AJ420784 Clostridi
	5	1268	39.1	110000	15	BA000016_01	Continuation (2 of
	6	1212.5	37.4	1887	2	BD074927	BD074927 Microbial
	7	1212.5	37.4	1887	2	AR210802	AR210802 Sequence
	8	1212.5	37.4	7018	8	AY452736	AY452736 Reporter
	9	1212.5	37.4	11846	8	AF354045	AF354045 Binary ve
	10	1212.5	37.4	11921	8	AF354046	AF354046 Binary ve
	11	1210.5	37.3	1806	2	AR428143	AR428143 Sequence
	12	1210.5	37.3	1809	8	AF354047	AF354047 Synthetic
	13	1210.5	37.3	1819	15	AF354044	AF354044 Staphyloc
	14	1210.5	37.3	1854	2	BD074926	BD074926 Microbial
	15	1210.5	37.3	1854	2	AR210801	AR210801 Sequence
	16	1210.5	37.3	2100	2	AR428142	AR428142 Sequence
	17	1210.5	37.3	6029	2	BD074925	BD074925 Microbial
	18	1210.5	37.3	6029	2	AR210800	AR210800 Sequence
c	19	1210.5	37.3	11096	2	CS106409	CS106409 Sequence
c	20	1210.5	37.3	15382	8	AY178047	AY178047 Expressio
c	21	1210.5	37.3	16368	8	AY178049	AY178049 Expressio
c	22	1210.5	37.3	16520	8	AY178048	AY178048 Expressio
	23	1209.5	37.3	8367	8	AY562545	AY562545 Binary Ve
	24	1209.5	37.3	9342	8	AY562544	AY562544 Binary Ve
c	25	1208.5	37.3	32798	2	CS108683	CS108683 Sequence
c	26	1208.5	37.3	32798	2	AR343138	AR343138 Sequence
c	27	1208.5	37.3	32798	2	AX382187	AX382187 Sequence
c	28	1208.5	37.3	33014	2	CS174971	CS174971 Sequence
c	29	1208.5	37.3	33014	2	CS196133	CS196133 Sequence
c	30	1208.5	37.3	33476	2	CS078955	CS078955 Sequence
c	31	1208.5	37.3	33476	2	CS223500	CS223500 Sequence
c	32	1208.5	37.3	33583	2	CS078953	CS078953 Sequence
c	33	1208.5	37.3	33583	2	CS223499	CS223499 Sequence
c	34	1208.5	37.3	33589	2	CS078954	CS078954 Sequence
c	35	1208.5	37.3	33589	2	CS223501	CS223501 Sequence
c	36	1208.5	37.3	36066	2	CS078956	CS078956 Sequence
c	37	1208.5	37.3	36066	2	CS223498	CS223498 Sequence
	38	1207.5	37.2	1812	2	BD002967	BD002967 Method fo
	39	1207.5	37.2	1812	15	S69414	S69414 uidA=beta-g
	40	1207.5	37.2	3035	2	AR030540	AR030540 Sequence
	41	1207.5	37.2	3824	2	AR030541	AR030541 Sequence
	42	1207.5	37.2	5667	8	AF502128	AF502128 Transient
	43	1207.5	37.2	5667	8	ECO414112	AJ414112 Cloning v
c	44	1207.5	37.2	6323	2	CS204337	CS204337 Sequence
c	45	1207.5	37.2	6928	8	AF433043	AF433043 Cloning v

```
GenCore version 5.1.8
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OM protein - nucleic search, using frame_plus_p2n model

Run on:          May 21, 2006, 20:02:43 ; Search time 869 Seconds
                                          (without alignments)
                                          7196.901 Million cell updates/sec

Title:           US-10-673-935-2
Perfect score:   3244
Sequence:        1 MESALYPIQNKYRFNTLMNG..........RDREPKDIAFTLKKRWQQLN 598

Scoring table:   BLOSUM62
                 Xgapop 10.0 , Xgapext  0.5
                 Ygapop 10.0 , Ygapext  0.5
                 Fgapop  6.0 , Fgapext  7.0
                 Delop   6.0 , Delext   7.0

Searched:        5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters:       10489840

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp
-Q=/abss/ABSSWEB_spool/US10673935/runat_19052006_150446_505/app_query.fasta_1
-DB=N_Geneseq -QFMT=fastap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss06p
-USER=US10673935_@CGN_1_1_1147_@runat_19052006_150446_505 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :       N_Geneseq_8:*
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                 2:  geneseqn1990s:*
                 3:  geneseqn2000s:*
                 4:  geneseqn2001as:*
                 5:  geneseqn2001bs:*
                 6:  geneseqn2002as:*
                 7:  geneseqn2002bs:*
                 8:  geneseqn2003as:*
                 9:  geneseqn2003bs:*
                 10:  geneseqn2003cs:*
                 11:  geneseqn2003ds:*
                 12:  geneseqn2004as:*
                 13:  geneseqn2004bs:*
                 14:  geneseqn2005s:*
                 15:  geneseqn2006s:*

        Pred. No. is the number of results predicted by chance to have a
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	3244	100.0	2150	6	AAL44836	Aal44836 L gasseri
	2	1212.5	37.4	1887	2	AAX23826	Aax23826 Bacillus
	3	1210.5	37.3	1806	3	AAA07931	Aaa07931 Staphyloc
	4	1210.5	37.3	1854	2	AAX23825	Aax23825 Bacillus
	5	1210.5	37.3	2100	3	AAA07930	Aaa07930 Staphyloc
	6	1210.5	37.3	6029	2	AAX23824	Aax23824 Bacillus
c	7	1210.5	37.3	11096	14	ADX38884	Adx38884 E. coli b
c	8	1210.5	37.3	12544	14	ADV50594	Adv50594 pDR10 vec
c	9	1208.5	37.3	32798	6	ABA97684	Aba97684 Replicati
c	10	1208.5	37.3	32798	14	AEA47146	Aea47146 Human TNF
c	11	1208.5	37.3	33014	13	ADP79484	Adp79484 Adenoviru
c	12	1208.5	37.3	33014	14	AED15875	Aed15875 Adenovira
c	13	1208.5	37.3	33014	14	AED87517	Aed87517 Adenovira
c	14	1208.5	37.3	33476	14	ADZ50987	Adz50987 Nucleotid
c	15	1208.5	37.3	33476	14	AEE09286	Aee09286 Clade B g
c	16	1208.5	37.3	33476	15	AEF88567	Aef88567 Adenovira
c	17	1208.5	37.3	33583	14	ADZ50985	Adz50985 Nucleotid
c	18	1208.5	37.3	33583	14	AEE09285	Aee09285 Clade A g
c	19	1208.5	37.3	33583	15	AEF88566	Aef88566 Adenovira
c	20	1208.5	37.3	33589	14	ADZ50986	Adz50986 Nucleotid
c	21	1208.5	37.3	33589	14	AEE09287	Aee09287 Clade C g
c	22	1208.5	37.3	33589	15	AEF88568	Aef88568 Adenovira
c	23	1208.5	37.3	36066	14	ADZ50988	Adz50988 Nucleotid
c	24	1208.5	37.3	36066	14	AEE09284	Aee09284 Clade B G
c	25	1208.5	37.3	36066	15	AEF88565	Aef88565 Adenovira
	26	1207.5	37.2	1809	6	ABK87080	Abk87080 uidA DNA
	27	1207.5	37.2	1812	8	ABT16606	Abt16606 Artificia
	28	1207.5	37.2	1812	10	ACC44709	Acc44709 E. coli b
	29	1207.5	37.2	1812	13	ADS46099	Ads46099 Bacterial
	30	1207.5	37.2	1812	14	AEB92290	Aeb92290 Beta-gluc
	31	1207.5	37.2	3035	2	AAV37748	Aav37748 PAT1 gene
	32	1207.5	37.2	3600	14	AED76834	Aed76834 QTPase RN
	33	1207.5	37.2	3600	15	AEE47052	Aee47052 Chimeric
	34	1207.5	37.2	3824	2	AAV37749	Aav37749 PAT1 gene
	35	1207.5	37.2	4051	14	AEB51403	Aeb51403 ACT12 der
c	36	1207.5	37.2	6323	14	AED84503	Aed84503 DNA for i
	37	1207.5	37.2	6389	14	ADY64147	Ady64147 Bioactive
	38	1207.5	37.2	8196	14	AEE48373	Aee48373 Expressio
	39	1207.5	37.2	8654	4	AAF80288	Aaf80288 Nucleotid
	40	1207.5	37.2	8654	4	AAF80285	Aaf80285 Nucleotid
	41	1207.5	37.2	8987	4	AAF80296	Aaf80296 Nucleotid
	42	1207.5	37.2	9390	4	AAF80292	Aaf80292 Nucleotid
	43	1207.5	37.2	9390	4	AAF80294	Aaf80294 Nucleotid
c	44	1207.5	37.2	10011	12	ADO07377	Ado07377 Plastid t
c	45	1207.5	37.2	10011	14	ADZ00019	Adz00019 Plasmid p

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OM protein - nucleic search, using frame_plus_p2n model

Run on: May 21, 2006, 20:19:43 ; Search time 300 Seconds
                                              (without alignments)
                                           5594.615 Million cell updates/sec

Title: US-10-673-935-2
Perfect score: 3244
Sequence: 1 MESALYPIQNKYRFNTLMNG.........RDREPKDIAFTLKKRWQQLN 598

Scoring table: BLOSUM62
                 Xgapop 10.0 , Xgapext   0.5
                 Ygapop 10.0 , Ygapext   0.5
                 Fgapop 6.0 , Fgapext   7.0
                 Delop   6.0 , Delext   7.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp
-Q=/abss/ABSSWEB_spool/US10673935/runat_19052006_150459_606/app_query.fasta_1
-DB=Issued_Patents_NA -QFMT=fastap -SUFFIX=p2n.rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-HOST=abss06p -USER=US10673935_@CGN_1_1_307_@runat_19052006_150459_606 -NCPU=6
-ICPU=3 -NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :   Issued_Patents_NA:*
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                 3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*
                 4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*
                 5: /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq:*
                 6: /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*
                 7: /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*
                 8: /EMC_Celerra_SIDS3/ptodata/2/ina/PP_COMB.seq:*
                 9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*
                 10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

       Pred. No. is the number of results predicted by chance to have a
       score greater than or equal to the score of the result being printed,
       and is derived by analysis of the total score distribution.

                              SUMMARIES
            %

	Result No.	Score	Query Match	Length	DB	ID	Description
	1	3244	100.0	2150	3	US-09-862-660-1	Sequence 1, Appli
	2	1212.5	37.4	1887	3	US-09-149-727-7	Sequence 7, Appli
	3	1210.5	37.3	1806	3	US-09-270-957-7	Sequence 7, Appli
	4	1210.5	37.3	1854	3	US-09-149-727-3	Sequence 3, Appli
	5	1210.5	37.3	2100	3	US-09-270-957-1	Sequence 1, Appli
	6	1210.5	37.3	6029	3	US-09-149-727-1	Sequence 1, Appli
c	7	1208.5	37.3	32798	3	US-09-604-694B-1	Sequence '1, Appli
	8	1207.5	37.2	3035	2	US-08-723-624-18	Sequence 18, Appl
	9	1207.5	37.2	3824	2	US-08-723-624-19	Sequence 19, Appl
	10	1202.5	37.1	3169	3	US-08-630-820-5	Sequence 5, Appli
	11	1202.5	37.1	3169	3	US-09-273-453-5	Sequence 5, Appli
	12	1200.5	37.0	4652	3	US-09-893-525-36	Sequence 36, Appl
	13	1200.5	37.0	5390	3	US-09-893-525-41	Sequence 41, Appl
	14	1200.5	37.0	5418	3	US-09-893-525-38	Sequence 38, Appl
c	15	1200.5	37.0	11978	3	US-09-792-568-8	Sequence 8, Appli
c	16	1200.5	37.0	12438	3	US-09-792-568-9	Sequence 9, Appli
	17	1199.5	37.0	1888	3	US-09-270-957-27	Sequence 27, Appl
	18	1191.5	36.7	8012	3	US-09-182-117-1	Sequence 1, Appli
	19	1191.5	36.7	8012	3	US-09-434-039A-1	Sequence 1, Appli
	20	1191.5	36.7	8418	3	US-09-182-117-5	Sequence 5, Appli
	21	1191.5	36.7	8418	3	US-09-434-039A-5	Sequence 5, Appli
	22	1191.5	36.7	8798	3	US-09-182-117-4	Sequence 4, Appli
	23	1191.5	36.7	8798	3	US-09-434-039A-4	Sequence 4, Appli
	24	1186	36.6	9335	3	US-09-097-319A-19	Sequence 19, Appl
	25	1186	36.6	9335	3	US-09-643-971-19	Sequence 19, Appl
	26	1184	36.5	4544	3	US-09-488-270A-1	Sequence 1, Appli
	27	1184	36.5	7742	2	US-08-882-704A-4	Sequence 4, Appli
	28	1184	36.5	7742	3	US-09-151-957-4	Sequence 4, Appli
	29	1184	36.5	7742	4	US-10-195-518-4	Sequence 4, Appli
	30	1184	36.5	9299	3	US-09-097-319A-15	Sequence 15, Appl
	31	1184	36.5	9299	3	US-09-643-971-15	Sequence 15, Appl
	32	1184	36.5	9408	3	US-09-097-319A-16	Sequence 16, Appl
	33	1184	36.5	9408	3	US-09-643-971-16	Sequence 16, Appl
	34	1183	36.5	2141	3	US-09-445-283C-27	Sequence 27, Appl
	35	1182	36.4	4947	3	US-09-118-276-21	Sequence 21, Appl
	36	1182	36.4	5642	2	US-08-318-772A-2	Sequence 2, Appli
	37	1182	36.4	5897	3	US-09-097-319A-26	Sequence 26, Appl
	38	1182	36.4	5897	3	US-09-643-971-26	Sequence 26, Appl
	39	1182	36.4	6898	3	US-09-097-319A-27	Sequence 27, Appl
	40	1182	36.4	6898	3	US-09-643-971-27	Sequence 27, Appl
	41	1182	36.4	10160	3	US-09-097-319A-8	Sequence 8, Appli
	42	1182	36.4	10160	3	US-09-643-971-8	Sequence 8, Appli
	43	1182	36.4	11784	3	US-09-097-319A-9	Sequence 9, Appli
	44	1182	36.4	11784	3	US-09-643-971-9	Sequence 9, Appli
	45	1182	36.4	11991	3	US-09-097-319A-10	Sequence 10, Appl

```
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OM protein - nucleic search, using frame_plus_p2n model

Run on:          May 21, 2006, 20:22:08 ; Search time 1898 Seconds
                                             (without alignments)
                                     *   5807.170 Million cell updates/sec


Title:           US-10-673-935-2
Perfect score:   3244
Sequence:        1 MESALYPIQNKYRFNTLMNG.........RDREPKDIAFTLKKRWQQLN 598


Scoring table:   BLOSUM62
                 Xgapop 10.0 , Xgapext  0.5
                 Ygapop 10.0 , Ygapext  0.5
                 Fgapop  6.0 , Fgapext  7.0
                 Delop   6.0 , Delext   7.0


Searched:        18892170 seqs, 6143817638 residues


Total number of hits satisfying chosen parameters:     37784340


Minimum DB seq length: 0
Maximum DB seq length: 2000000000


Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries


Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/abss/ABSSWEB_spool/US10673935/runat_19052006_150504_661/app_query.fasta_1
-DB=Published_Applications_NA_Main -QFMT=fastap -SUFFIX=p2n.rnpbm
-MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1
-MATRIX=blosum62 -TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct
-THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext
-HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss04
-USER=US10673935_@CGN_1_1_1675_@runat_19052006_150504_661 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7


Database :       Published_Applications_NA_Main:*
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                 3:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
                 4:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
                 5:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
                 6:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
                 7:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
                 8:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
                 9:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
                 10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
                 11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
                 12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
                 13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
                 14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
                 15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*
                 16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	3244	100.0	2150	3	US-09-862-660-1	Sequence 1, Appli
	2	3244	100.0	2150	8	US-10-673-935-1	Sequence 1, Appli
	3	1212.5	37.4	1887	7	US-10-120-145-7	Sequence 7, Appli
	4	1212.5	37.4	3651	7	US-10-322-656-45	Sequence 45, Appl
	5	1212.5	37.4	4084	7	US-10-322-656-48	Sequence 48, Appl
	6	1210.5	37.3	1806	7	US-10-364-649-7	Sequence 7, Appli
	7	1210.5	37.3	1854	7	US-10-120-145-3	Sequence 3, Appli
	8	1210.5	37.3	2100	7	US-10-364-649-1	Sequence 1, Appli
	9	1210.5	37.3	6029	7	US-10-120-145-1	Sequence 1, Appli
c	10	1210.5	37.3	11096	9	US-10-872-156-9	Sequence 9, Appli
c	11	1210.5	37.3	11096	16	US-11-238-025-9	Sequence 9, Appli
c	12	1208.5	37.3	32798	7	US-10-424-638-1	Sequence 1, Appli
c	13	1208.5	37.3	33014	13	US-11-138-931-1	Sequence 1, Appli
c	14	1208.5	37.3	33014	15	US-11-077-716-1	Sequence 1, Appli
	15	1207.5	37.2	1809	8	US-10-432-777-16	Sequence 16, Appl
	16	1207.5	37.2	1812	7	US-10-161-403-105	Sequence 105, App
	17	1207.5	37.2	1812	7	US-10-369-493-24529	Sequence 24529, A
	18	1207.5	37.2	1812	9	US-10-161-408-16	Sequence 16, Appl
	19	1207.5	37.2	1812	10	US-10-161-408-16	Sequence 16, Appl
	20	1207.5	37.2	1812	13	US-11-006-076-105	Sequence 105, App
	21	1207.5	37.2	1812	16	US-11-082-154A-105	Sequence 105, App
	22	1207.5	37.2	4051	13	US-11-038-900-20	Sequence 20, Appl
	23	1207.5	37.2	8654	3	US-09-845-064-11	Sequence 11, Appl
	24	1207.5	37.2	8654	3	US-09-845-064-14	Sequence 14, Appl
	25	1207.5	37.2	8987	3	US-09-845-064-22	Sequence 22, Appl
	26	1207.5	37.2	9285	3	US-09-845-064-52	Sequence 52, Appl
	27	1207.5	37.2	9390	3	US-09-845-064-18	Sequence 18, Appl
	28	1207.5	37.2	9390	3	US-09-845-064-20	Sequence 20, Appl
	29	1207.5	37.2	9688	3	US-09-845-064-50	Sequence 50, Appl
c	30	1207.5	37.2	10011	8	US-10-680-824A-19	Sequence 19, Appl
c	31	1207.5	37.2	10011	10	US-10-957-562-4	Sequence 4, Appli
	32	1207.5	37.2	15077	3	US-09-845-064-57	Sequence 57, Appl
c	33	1207.5	37.2	15208	3	US-09-845-064-51	Sequence 51, Appl
	34	1205.5	37.2	5898	9	US-10-640-422-160	Sequence 160, App
c	35	1205.5	37.2	5919	10	US-10-169-050-21	Sequence 21, Appl
	36	1205.5	37.2	7510	11	US-10-527-048-19	Sequence 19, Appl
	37	1205.5	37.2	8327	11	US-10-527-048-23	Sequence 23, Appl
	38	1205.5	37.2	12224	7	US-10-336-566-83	Sequence 83, Appl
	39	1205.5	37.2	12225	8	US-10-646-628-1	Sequence 1, Appli
	40	1204.5	37.1	3451	7	US-10-161-403-108	Sequence 108, App
	41	1204.5	37.1	3451	9	US-10-161-408-20	Sequence 20, Appl
	42	1204.5	37.1	3451	10	US-10-161-408-20	Sequence 20, Appl
	43	1204.5	37.1	3451	13	US-11-006-076-108	Sequence 108, App
	44	1204.5	37.1	3451	16	US-11-082-154A-108	Sequence 108, App
	45	1204.5	37.1	14627	7	US-10-161-403-109	Sequence 109, App

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OM protein - nucleic search, using frame_plus_p2n model

Run on: May 21, 2006, 20:30:19 ; Search time 51 Seconds
                                              (without alignments)
                                              1240.954 Million cell updates/sec

Title: US-10-673-935-2
Perfect score: 3244
Sequence: 1 MESALYPIQNKYRFNTLMNG..........RDREPKDIAFTLKKRWQQLN 598

Scoring table: BLOSUM62
                    Xgapop 10.0 , Xgapext 0.5
                    Ygapop 10.0 , Ygapext 0.5
                    Fgapop 6.0 , Fgapext 7.0
                    Delop   6.0 , Delext   7.0

Searched: 224314 seqs, 35277956 residues

Total number of hits satisfying chosen parameters: 448628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp
-Q=/abss/ABSSWEB_spool/US10673935/runat_19052006_150510_727/app_query.fasta_1
-DB=Published_Applications_NA_New -QFMT=fastap -SUFFIX=p2n.rnpbn -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -HOST=abss05p
-USER=US10673935_@CGN_1_1_20_@runat_19052006_150510_727 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :   Published_Applications_NA_New:*
                    1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09_NEW_PUB.seq:*
                    2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US06_NEW_PUB.seq:*
                    3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_NEW_PUB.seq:*
                    4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_NEW_PUB.seq:*
                    5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
                    6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10_NEW_PUB.seq:*
                    7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq:*
                    8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US60_NEW_PUB.seq:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
                         %
Result   Query

	No.	Score	Match	Length	DB	ID	Description
	1	1182	36.4	8953	7	US-11-185-301-10	Sequence 10, Appl
	2	1182	36.4	8953	7	US-11-264-784-113	Sequence 113, App
	3	1157	35.7	12290	6	US-10-946-650-59	Sequence 59, Appl
	4	1157	35.7	13383	6	US-10-946-650-61	Sequence 61, Appl
	5	953	29.4	2191	6	US-10-511-937-335	Sequence 335, App
	6	414.5	12.8	3075	7	US-11-226-605-51	Sequence 51, Appl
	7	414.5	12.8	3157	6	US-10-468-193-29	Sequence 29, Appl
	8	356.5	11.0	2031	7	US-11-256-428-8	Sequence 8, Appli
	9	348.5	10.7	2201	7	US-11-256-428-5	Sequence 5, Appli
	10	336.5	10.4	2031	7	US-11-256-428-6	Sequence 6, Appli
	11	336.5	10.4	3159	7	US-11-256-428-7	Sequence 7, Appli
	12	246.5	7.6	7408	7	US-11-245-473-13	Sequence 13, Appl
	13	186	5.7	563	6	US-10-488-619-1350	Sequence 1350, Ap
	14	167.5	5.2	491	6	US-10-511-937-3084	Sequence 3084, Ap
c	15	152.5	4.7	712	6	US-10-488-619-1349	Sequence 1349, Ap
	16	150.5	4.6	250	7	US-11-136-524-103	Sequence 103, App
	17	136	4.2	2865	7	US-11-217-529-75625	Sequence 75625, A
	18	119.5	3.7	2466	7	US-11-217-529-78674	Sequence 78674, A
	19	110	3.4	3453	7	US-11-217-529-2848	Sequence 2848, Ap
	20	107	3.3	2289	7	US-11-217-529-2123	Sequence 2123, Ap
	21	107	3.3	3306	7	US-11-217-529-78513	Sequence 78513, A
	22	106.5	3.3	1596	7	US-11-217-529-82291	Sequence 82291, A
	23	105.5	3.3	1866	7	US-11-217-529-4625	Sequence 4625, Ap
	24	105	3.2	2526	7	US-11-217-529-1313	Sequence 1313, Ap
	25	104.5	3.2	1836	7	US-11-217-529-82281	Sequence 82281, A
	26	104.5	3.2	1938	7	US-11-217-529-3036	Sequence 3036, Ap
	27	104	3.2	1890	7	US-11-217-529-1600	Sequence 1600, Ap
	28	102.5	3.2	2256	7	US-11-217-529-75912	Sequence 75912, A
	29	102.5	3.2	3495	7	US-11-217-529-5994	Sequence 5994, .Ap
	30	102	3.1	3378	7	US-11-217-529-82474	Sequence 82474, A
	31	101.5	3.1	2034	7	US-11-217-529-77966	Sequence 77966, A
	32	101.5	3.1	2997	7	US-11-217-529-80519	Sequence 80519, A
	33	101	3.1	1512	7	US-11-217-529-4478	Sequence 4478, Ap
	34	101	3.1	1656	7	US-11-217-529-3536	Sequence 3536, Ap
	35	101	3.1	3819	7	US-11-217-529-78626	Sequence 78626, A
	36	101	3.1	12783	7	US-11-217-529-4700	Sequence 4700, Ap
	37	100.5	3.1	2082	7	US-11-217-529-75578	Sequence 75578, A
	38	100.5	3.1	2343	7	US-11-217-529-4231	Sequence 4231, Ap
	39	100	3.1	1241	7	US-11-136-524-16	Sequence 16, Appl
	40	100	3.1	2691	7	US-11-217-529-78902	Sequence 78902, A
	41	99.5	3.1	1626	7	US-11-217-529-75408	Sequence 75408, A
	42	99.5	3.1	2007	7	US-11-217-529-5555	Sequence 5555, Ap
	43	99.5	3.1	11564	6	US-10-505-928-105	Sequence 105, App
	44	99	3.1	1728	7	US-11-217-529-77037	Sequence 77037, A
	45	99	3.1	2586	7	US-11-217-529-3103	Sequence 3103, Ap

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OM protein - nucleic search, using frame_plus_p2n model

Run on:           May 21, 2006, 20:18:42 ; Search time 7655 Seconds
                                          (without alignments)
                                          6552.533 Million cell updates/sec

Title:            US-10-673-935-2
Perfect score:    3244
Sequence:         1 MESALYPIQNKYRFNTLMNG..........RDREPKDIAFTLKKRWQQLN 598

Scoring table:    BLOSUM62
                  Xgapop 10.0 , Xgapext  0.5
                  Ygapop 10.0 , Ygapext  0.5
                  Fgapop  6.0 , Fgapext  7.0
                  Delop   6.0 , Delext   7.0

Searched:         48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters:      96473596

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/abss/ABSSWEB_spool/US10673935/runat_19052006_150454_558/app_query.fasta_1
-DB=EST -QFMT=fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss04
-USER=US10673935_@CGN_1_1_6323_@runat_19052006_150454_558 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :        EST:*
                  1:  gb_est1:*
                  2:  gb_est3:*
                  3:  gb_est4:*
                  4:  gb_est5:*
                  5:  gb_est6:*
                  6:  gb_htc:*
                  7:  gb_est2:*
                  8:  gb_est7:*
                  9:  gb_est8:*
                  10: gb_est9:*
                  11: gb_gss1:*
                  12: gb_gss2:*
                  13: gb_gss3:*
                  14: gb_gss4:*

          Pred. No. is the number of results predicted by chance to have a
          score greater than or equal to the score of the result being printed,
```

and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	939	28.9	2229	6	CR859852	CR859852 Pongo pyg
	2	936	28.9	2257	6	CR860821	CR860821 Pongo pyg
	3	908	28.0	2431	6	AK159526	AK159526 Mus muscu
	4	908	28.0	2456	6	AK162436	AK162436 Mus muscu
	5	908	28.0	2457	6	AK150048	AK150048 Mus muscu
	6	908	28.0	2512	6	AK136519	AK136519 Mus muscu
	7	906	27.9	2456	6	AK159163	AK159163 Mus muscu
	8	906	27.9	2456	6	AK159804	AK159804 Mus muscu
	9	897	27.7	2457	6	AK151802	AK151802 Mus muscu
	10	897	27.7	2457	6	AK152206	AK152206 Mus muscu
	11	895	27.6	2675	6	AK146247	AK146247 Mus muscu
	12	893	27.5	2473	6	AY321342	AY321342 Rattus no
	13	889	27.4	2095	4	CD014094	CD014094 90135027
	14	888.5	27.4	2445	6	AK159564	AK159564 Mus muscu
	15	813	25.1	1995	4	CD014092	CD014092 90134967
	16	775.5	23.9	2274	6	AK041058	AK041058 Mus muscu
	17	734.5	22.6	1853	4	CD014093	CD014093 90135266
	18	692	21.3	1377	6	CR593823	CR593823 full-leng
	19	631	19.5	1124	5	CD503076	CD503076 CDA60-C07
	20	613.5	18.9	1446	6	AK149814	AK149814 Mus muscu
	21	608.5	18.8	1138	5	CD503098	CD503098 CDA60-D07
	22	591	18.2	1959	14	DQ045133	DQ045133 Homo sapi
	23	569	17.5	906	3	BQ941196	BQ941196 AGENCOURT
	24	553	17.0	1092	10	DW042175	DW042175 CFW300-C1
c	25	550.5	17.0	921	13	CL486845	CL486845 SAIL_443_
	26	544	16.8	878	8	CN155220	CN155220 942501 MA
	27	540	16.6	1051	4	BX363460	BX363460 BX363460
	28	539.5	16.6	1107	10	DV013446	DV013446 CNB280-D0
	29	519.5	16.0	1105	9	DR125834	DR125834 49066605
c	30	518.5	16.0	857	4	BX745933	BX745933 BX745933
	31	513	15.8	846	4	CA453907	CA453907 AGENCOURT
	32	510	15.7	914	4	CB203472	CB203472 AGENCOURT
	33	508	15.7	739	4	BX618136	BX618136 BX618136
	34	501	15.4	775	9	DN875774	DN875774 nae01g08.
c	35	497.5	15.3	1063	4	BX401772	BX401772 BX401772
	36	487.5	15.0	816	5	CK467358	CK467358 938649 MA
	37	483.5	14.9	791	3	BU239978	BU239978 603323761
	38	482	14.9	740	5	CF521612	CF521612 AGENCOURT
	39	480.5	14.8	811	13	CL679241	CL679241 PRI0125c_
	40	480.5	14.8	832	10	DT271332	DT271332 JGI_CAAV4
	41	477.5	14.7	900	4	CA489317	CA489317 AGENCOURT
	42	473.5	14.6	879	10	DT815232	DT815232 LB01626.C
	43	468	14.4	767	5	CF255373	CF255373 mdvn127_c
	44	467.5	14.4	799	3	BU366987	BU366987 603585124
	45	467	14.4	1055	3	BM557676	BM557676 AGENCOURT

```
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OM protein - protein search, using sw model

Run on:          May 20, 2006, 09:07:48 ; Search time 198 Seconds
                                          (without alignments)
                                 1380.886 Million cell updates/sec

Title:           US-10-673-935-2
Perfect score:   3244
Sequence:        1 MESALYPIQNKYRFNTLMNG..........RDREPKDIAFTLKKRWQQLN 598

Scoring table:   BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched:        2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters:       2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       A_Geneseq_8:*
                 1:  geneseqp1980s:*
                 2:  geneseqp1990s:*
                 3:  geneseqp2000s:*
                 4:  geneseqp2001s:*
                 5:  geneseqp2002s:*
                 6:  geneseqp2003as:*
                 7:  geneseqp2003bs:*
                 8:  geneseqp2004s:*
                 9:  geneseqp2005s:*
                 10:  geneseqp2006s:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

                             SUMMARIES
                     %
Result               Query
  No.    Score    Match Length DB   ID                    Description
-----------------------------------------------------------------------------
     1    3244    100.0    598  5   AAM48998              Aam48998 L gasseri
     2    3244    100.0    598  9   AEB18199              Aeb18199 Lactobaci
     3    1212.5   37.4    615  3   AAB28408              Aab28408 Codon-opt
     4    1210.5   37.3    602  2   AAW93825              Aaw93825 Bacillus
     5    1210.5   37.3    602  2   AAW93822              Aaw93822 Bacillus
     6    1210.5   37.3    602  2   AAW93826              Aaw93826 Bacillus
     7    1210.5   37.3    602  3   AAB28402              Aab28402 Staphyloc
     8    1210.5   37.3    618  2   AAW93821              Aaw93821 Bacillus
     9    1207.5   37.2    603  2   AAW93827              Aaw93827 E. coli G
    10    1207.5   37.2    603  2   AAW93824              Aaw93824 Human GUS
    11    1207.5   37.2    603  3   AAB28431              Aab28431 Human bet
    12    1207.5   37.2    603  6   ABP96657              Abp96657 E. coli b
```

13	1207.5	37.2	603	6	ABJ19649	Abj19649 Artificia
14	1207.5	37.2	603	8	ADN18189	Adn18189 Bacterial
15	1207.5	37.2	603	9	AEB18200	Aeb18200 Escherich
16	1205.5	37.2	603	5	ABB84108	Abb84108 GUS prote
17	1205.5	37.2	618	7	ADL01666	Adl01666 Modified
18	1205.5	37.2	1010	3	AAY68840	Aay68840 Fusion pr
19	1201.5	37.0	604	9	AEB18201	Aeb18201 Staphyloc
20	1200.5	37.0	604	7	ADD27986	Add27986 Beta-gluc
21	1200.5	37.0	604	8	ADS54300	Ads54300 Beta-gluc
22	1200.5	37.0	659	7	ADD27989	Add27989 Oleosin/b
23	1200.5	37.0	659	8	ADS54303	Ads54303 Oleosin-b
24	1200.5	37.0	850	7	ADD27991	Add27991 Caleosin/
25	1200.5	37.0	850	8	ADS54305	Ads54305 Caleosin-
26	1198.5	36.9	603	5	ABB84107	Abb84107 GUS prote
27	1195.5	36.9	602	2	AAW93820	Aaw93820 Bacillus
28	1195.5	36.9	832	2	AAW04302	Aaw04302 Antibody/
29	1189	36.7	711	6	ABR83626	Abr83626 SUMO-beta
30	1184	36.5	602	2	AAW42429	Aaw42429 Escherich
31	1184	36.5	1242	5	ABB81108	Abb81108 LUC-U3'-U
32	1184	36.5	1242	6	ABB84637	Abb84637 LUC-U3'-U
33	1183.5	36.5	602	3	AAB28409	Aab28409 Salmonell
34	1182	36.4	602	2	AAR43387	Aar43387 Beta-gluc
35	1182	36.4	607	8	ADS26258	Ads26258 Bacterial
36	1174	36.2	602	1	AAP82948	Aap82948 Beta-gluc
37	1163	35.9	608	9	AED17404	Aed17404 E. coli B
38	1163	35.9	608	9	AED68746	Aed68746 beta-gluc
39	1163	35.9	608	10	AEF40107	Aef40107 E. coli H
40	1156.5	35.7	617	4	AAU39683	Aau39683 Propionib
41	1156.5	35.7	617	6	ABM36202	Abm36202 Propionib
42	1143	35.2	615	9	AEB18221	Aeb18221 Scopulari
43	1143	35.2	641	9	AEB18180	Aeb18180 Scopulari
44	1136	35.0	599	8	ADV89677	Adv89677 Streptoco
45	1136	35.0	599	8	ADV83078	Adv83078 Streptoco

```
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OM protein - protein search, using sw model

Run on:           May 20, 2006, 09:16:38 ; Search time 50 Seconds
                                            (without alignments)
                                            1046.866 Million cell updates/sec

Title:            US-10-673-935-2
Perfect score:    3244
Sequence:         1 MESALYPIQNKYRFNTLMNG..........RDREPKDIAFTLKKRWQQLN 598

Scoring table:    BLOSUM62
                  Gapop 10.0 , Gapext 0.5

Searched:         650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters:        650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :        Issued_Patents_AA:*
                  1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:*
                  2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*
                  3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
                  4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
                  5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*
                  6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
                  7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

                              SUMMARIES
                      %
Result            Query
   No.    Score   Match Length DB  ID                        Description
--------------------------------------------------------------------------------
       1    3244  100.0    598  2  US-09-862-660-2           Sequence 2, Appli
       2  1212.5   37.4    607  2  US-09-149-727-8           Sequence 8, Appli
       3  1212.5   37.4    607  2  US-09-270-957-18          Sequence 18, Appl
       4  1212.5   37.4    615  2  US-09-270-957-28          Sequence 28, Appl
       5  1210.5   37.3    602  2  US-09-149-727-2           Sequence 2, Appli
       6  1210.5   37.3    602  2  US-09-270-957-2           Sequence 2, Appli
       7  1210.5   37.3    602  2  US-09-270-957-8           Sequence 8, Appli
       8  1210.5   37.3    602  2  US-09-270-957-15          Sequence 15, Appl
       9  1210.5   37.3    618  2  US-09-149-727-4           Sequence 4, Appli
      10  1207.5   37.2    603  2  US-09-149-727-6           Sequence 6, Appli
      11  1207.5   37.2    603  2  US-09-270-957-17          Sequence 17, Appl
      12  1207.5   37.2    603  2  US-09-270-957-23          Sequence 23, Appl
      13  1205.5   37.2   1010  2  US-09-118-276-12          Sequence 12, Appl
      14  1202.5   37.1    832  2  US-08-630-820-7           Sequence 7, Appli
      15  1202.5   37.1    832  2  US-09-273-453-7           Sequence 7, Appli
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16	1200.5	37.0	604	2	US-09-893-525-37	Sequence 37, Appl
17	1200.5	37.0	659	2	US-09-893-525-40	Sequence 40, Appl
18	1200.5	37.0	850	2	US-09-893-525-42	Sequence 42, Appl
19	1184	36.5	602	1	US-08-882-704A-5	Sequence 5, Appli
20	1184	36.5	602	2	US-09-151-957-5	Sequence 5, Appli
21	1184	36.5	602	2	US-10-195-518-5	Sequence 5, Appli
22	1184	36.5	602	7	5432081-2	Patent No. 5432081
23	1184	36.5	1242	2	US-09-488-270A-2	Sequence 2, Appli
24	1161	35.8	600	7	5268463-2	Patent No. 5268463
25	953	29.4	613	2	US-09-149-727-5	Sequence 5, Appli
26	953	29.4	613	2	US-09-270-957-16	Sequence 16, Appl
27	953	29.4	651	2	US-09-715-858-2	Sequence 2, Appli
28	919.5	28.3	563	2	US-09-270-957-6	Sequence 6, Appli
29	919.5	28.3	563	2	US-09-270-957-21	Sequence 21, Appl
30	908	28.0	648	2	US-09-715-858-4	Sequence 4, Appli
31	816.5	25.2	376	2	US-09-270-957-4	Sequence 4, Appli
32	816.5	25.2	376	2	US-09-270-957-19	Sequence 19, Appl
33	680.5	21.0	500	2	US-09-949-016-11697	Sequence 11697, A
34	655	20.2	372	2	US-09-270-957-3	Sequence 3, Appli
35	655	20.2	372	2	US-09-270-957-22	Sequence 22, Appl
36	581.5	17.9	535	2	US-09-270-957-20	Sequence 20, Appl
37	573	17.7	540	2	US-09-270-957-5	Sequence 5, Appli
38	542	16.7	282	2	US-09-634-238-345	Sequence 345, App
39	421.5	13.0	1031	2	US-09-489-039A-11186	Sequence 11186, A
40	416.5	12.8	1334	7	5476657-1	Patent No. 5476657
41	415.5	12.8	1403	1	US-08-694-865-17	Sequence 17, Appl
42	415.5	12.8	1403	2	US-09-124-491-17	Sequence 17, Appl
43	415.5	12.8	1403	2	US-09-383-912-17	Sequence 17, Appl
44	414.5	12.8	1010	2	US-09-654-449-2	Sequence 2, Appli
45	414.5	12.8	1010	2	US-09-759-152A-2	Sequence 2, Appli

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OM protein - protein search, using sw model

Run on: May 20, 2006, 09:17:23 ; Search time 184 Seconds
                                                (without alignments)
                                            1505.448 Million cell updates/sec

Title: US-10-673-935-2
Perfect score: 3244
Sequence: 1 MESALYPIQNKYRFNTLMNG..........RDREPKDIAFTLKKRWQQLN 598

Scoring table: BLOSUM62
                   Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Published_Applications_AA_Main:*
                   1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
                   2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
                   3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
                   4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
                   5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
                   6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

          Pred. No. is the number of results predicted by chance to have a
          score greater than or equal to the score of the result being printed,
          and is derived by analysis of the total score distribution.

                                SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	3244	100.0	598	3	US-09-862-660-2	Sequence 2, Appli
2	3244	100.0	598	4	US-10-673-935-2	Sequence 2, Appli
3	3244	100.0	598	5	US-10-757-093-21	Sequence 21, Appl
4	1212.5	37.4	607	4	US-10-120-145-8	Sequence 8, Appli
5	1212.5	37.4	607	4	US-10-364-649-18	Sequence 18, Appl
6	1212.5	37.4	615	4	US-10-364-649-28	Sequence 28, Appl
7	1210.5	37.3	602	4	US-10-120-145-2	Sequence 2, Appli
8	1210.5	37.3	602	4	US-10-364-649-2	Sequence 2, Appli
9	1210.5	37.3	602	4	US-10-364-649-8	Sequence 8, Appli
10	1210.5	37.3	602	4	US-10-364-649-15	Sequence 15, Appl
11	1210.5	37.3	602	5	US-10-757-093-23	Sequence 23, Appl
12	1210.5	37.3	618	4	US-10-120-145-4	Sequence 4, Appli
13	1207.5	37.2	603	4	US-10-161-403-106	Sequence 106, App
14	1207.5	37.2	603	4	US-10-120-145-6	Sequence 6, Appli
15	1207.5	37.2	603	4	US-10-364-649-17	Sequence 17, Appl
16	1207.5	37.2	603	4	US-10-364-649-23	Sequence 23, Appl

17	1207.5	37.2	603	4	US-10-369-493-842	Sequence 842, App
18	1207.5	37.2	603	4	US-10-161-408-17	Sequence 17, Appl
19	1207.5	37.2	603	5	US-10-757-093-22	Sequence 22, Appl
20	1207.5	37.2	603	5	US-10-161-408-17	Sequence 17, Appl
21	1207.5	37.2	603	6	US-11-006-076-106	Sequence 106, App
22	1207.5	37.2	603	6	US-11-082-154A-106	Sequence 106, App
23	1205.5	37.2	618	4	US-10-356-088-28	Sequence 28, Appl
24	1205.5	37.2	618	4	US-10-799-326-28	Sequence 28, Appl
25	1205.5	37.2	1010	3	US-09-118-276-12	Sequence 12, Appl
26	1205.5	37.2	1010	4	US-10-705-197A-12	Sequence 12, Appl
27	1202.5	37.1	832	5	US-10-632-815-7	Sequence 7, Appli
28	1200.5	37.0	604	3	US-09-893-525-37	Sequence 37, Appl
29	1200.5	37.0	604	4	US-10-763-380-37	Sequence 37, Appl
30	1200.5	37.0	659	3	US-09-893-525-40	Sequence 40, Appl
31	1200.5	37.0	659	4	US-10-763-380-40	Sequence 40, Appl
32	1200.5	37.0	850	3	US-09-893-525-42	Sequence 42, Appl
33	1200.5	37.0	850	4	US-10-763-380-42	Sequence 42, Appl
34	1189	36.7	711	4	US-10-338-411-23	Sequence 23, Appl
35	1189	36.7	711	4	US-10-389-640-23	Sequence 23, Appl
36	1184	36.5	602	4	US-10-195-518-5	Sequence 5, Appli
37	1182	36.4	607	4	US-10-369-493-15291	Sequence 15291, A
38	1163	35.9	608	6	US-11-085-864-2	Sequence 2, Appli
39	1163	35.9	608	6	US-11-127-004-2	Sequence 2, Appli
40	1163	35.9	608	6	US-11-190-408-2	Sequence 2, Appli
41	1143	35.2	641	5	US-10-757-093-2	Sequence 2, Appli
42	1108.5	34.2	644	5	US-10-757-093-10	Sequence 10, Appl
43	1092.5	33.7	612	5	US-10-757-093-8	Sequence 8, Appli
44	1077.5	33.2	634	5	US-10-757-093-4	Sequence 4, Appli
45	1065.5	32.8	634	5	US-10-757-093-6	Sequence 6, Appli

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OM protein - protein search, using sw model

Run on: May 20, 2006, 09:18:23 ; Search time 10 Seconds
                                         (without alignments)
                                         127.740 Million cell updates/sec

Title: US-10-673-935-2
Perfect score: 3244
Sequence: 1 MESALYPIQNKYRFNTLMNG.........RDREPKDIAFTLKKRWQQLN 598

Scoring table: BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched: 21570 seqs, 2136119 residues

Total number of hits satisfying chosen parameters: 21570

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Published_Applications_AA_New:*
                 1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
                 2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
                 3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
                 4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
                 5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
                 6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
                 7: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
                 8: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	953	29.4	651	6	US-10-511-937-2401	Sequence 2401, Ap
2	99.5	3.1	3460	6	US-10-505-928-104	Sequence 104, App
3	92.5	2.9	1395	6	US-10-505-928-513	Sequence 513, App
4	91.5	2.8	688	6	US-10-514-738-33	Sequence 33, Appl
5	91.5	2.8	766	6	US-10-514-738-2	Sequence 2, Appli
6	91.5	2.8	766	6	US-10-514-738-4	Sequence 4, Appli
7	91.5	2.8	766	6	US-10-514-738-35	Sequence 35, Appl
8	89.5	2.8	967	6	US-10-505-928-795	Sequence 795, App
9	87.5	2.7	1722	6	US-10-505-928-780	Sequence 780, App
10	85	2.6	643	7	US-11-261-390-13	Sequence 13, Appl
11	84.5	2.6	811	6	US-10-196-749-414	Sequence 414, App
12	84	2.6	1085	6	US-10-505-928-343	Sequence 343, App
13	83	2.6	1531	6	US-10-505-928-217	Sequence 217, App
14	82.5	2.5	788	6	US-10-485-346-2	Sequence 2, Appli

15	82	2.5	579	7	US-11-261-390-15	Sequence 15, Appl
16	80.5	2.5	642	6	US-10-505-928-259	Sequence 259, App
17	80.5	2.5	647	7	US-11-312-958-58	Sequence 58, Appl
18	78.5	2.4	258	6	US-10-490-953-15	Sequence 15, Appl
19	78	2.4	582	7	US-11-301-554-334	Sequence 334, App
20	78	2.4	1842	6	US-10-511-937-2929	Sequence 2929, Ap
21	77	2.4	417	6	US-10-511-937-2594	Sequence 2594, Ap
22	77	2.4	943	7	US-11-302-678-29	Sequence 29, Appl
23	76.5	2.4	1151	7	US-11-246-999-103	Sequence 103, App
24	76	2.3	910	7	US-11-301-924-16	Sequence 16, Appl
25	75.5	2.3	760	6	US-10-514-_738-37	Sequence 37, Appl
26	75	2.3	600	6	US-10-370-959-155	Sequence 155, App
27	75	2.3	1457	7	US-11-280-757-37	Sequence 37, Appl
28	75	2.3	2351	7	US-11-183-218-30	Sequence 30, Appl
29	75	2.3	2351	7	US-11-280-757-35	Sequence 35, Appl
30	74.5	2.3	491	6	US-10-511-937-2602	Sequence 2602, Ap
31	74.5	2.3	1186	6	US-10-511-937-2566	Sequence 2566, Ap
32	74	2.3	400	6	US-10-490-953-20	Sequence 20, Appl
33	74	2.3	437	6	US-10-504-120-32	Sequence 32, Appl
34	74	2.3	501	6	US-10-511-937-3005	Sequence 3005, Ap
35	74	2.3	575	7	US-11-230-593A-29	Sequence 29, Appl
36	74	2.3	750	6	US-10-196-749-104	Sequence 104, App
37	74	2.3	4590	6	US-10-505-928-569	Sequence 569, App
38	73.5	2.3	361	6	US-10-733-816-3	Sequence 3, Appli
39	73.5	2.3	394	6	US-10-733-816-2	Sequence 2, Appli
40	73.5	2.3	420	6	US-10-733-816-1	Sequence 1, Appli
41	73.5	2.3	443	6	US-10-196-749-516	Sequence 516, App
42	73.5	2.3	493	7	US-11-315-766-29	Sequence 29, Appl
43	73.5	2.3	737	6	US-10-505-928-608	Sequence 608, App
44	73.5	2.3	750	6	US-10-511-937-2413	Sequence 2413, Ap
45	73	2.3	371	6	US-10-370-959-147	Sequence 147, App

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OM protein - protein search, using sw model

Run on:          May 20, 2006, 09:11:33 ; Search time 42 Seconds
                                            (without alignments)
                                          1369.943 Million cell updates/sec

Title:           US-10-673-935-2
Perfect score:   3244
Sequence:        1 MESALYPIQNKYRFNTLMNG.........RDREPKDIAFTLKKRWQQLN 598

Scoring table:   BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched:        283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters:       283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       PIR_80:*
                 1:  pir1:*
                 2:  pir2:*
                 3:  pir3:*
                 4:  pir4:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.
```

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1207.5	37.2	603	1	GBECGC	beta-glucuronidase
2	953	29.4	651	2	A26581	beta-glucuronidase
3	917.5	28.3	563	2	A72300	beta-glucuronidase
4	916	28.2	648	2	A25047	beta-glucuronidase
5	908	28.0	648	2	A32576	beta-glucuronidase
6	850	26.2	370	2	D90919	beta-D-glucuronida
7	848	26.1	368	2	A85768	partial beta-D-glu
8	822.5	25.4	570	2	C90485	beta-glucuronidase
9	480	14.8	716	2	JU0275	beta-galactosidase
10	463	14.3	755	2	D95842	probable beta-gala
11	457	14.1	1087	2	F72283	beta-galactosidase
12	420	12.9	1014	2	C83990	beta-galactosidase
13	414.5	12.8	1024	1	GBEC	beta-galactosidase
14	414.5	12.8	1024	2	E90678	beta-D-galactosida
15	414.5	12.8	1024	2	A85529	beta-D-galactosida
16	399.5	12.3	996	2	D86872	beta-galactosidase
17	399	12.3	1034	2	T30574	beta-galactosidase
18	380	11.7	626	2	A42891	beta-galactosidase

19	377.5	11.6	1007	2	A30093	beta-galactosidase
20	376.5	11.6	1026	2	A49750	beta-galactosidase
21	372	11.5	1025	1	JC1266	beta-galactosidase
22	368.5	11.4	1034	2	T30551	beta-galactosidase
23	367	11.3	897	2	A39405	beta-galactosidase
24	359	11.1	1060	2	AI0201	beta-galactosidase
25	354.5	10.9	237	2	E90919	interrupted beta-D
26	354.5	10.9	237	2	B85768	partial beta-D-glu
27	351	10.8	1075	2	T47603	beta Galactosidase
28	342	10.5	1042	1	GBECE	beta-galactosidase
29	342	10.5	1042	2	E85968	evolved beta-D-gal
30	342	10.5	1042	2	F91123	evolved beta-D-gal
31	340	10.5	1005	2	T31333	beta-galactosidase
32	330	10.2	1307	2	T35944	probable beta-gala
33	319	9.8	1034	2	A24925	beta-galactosidase
34	314	9.7	1015	2	I39697	beta-galactosidase
35	268.5	8.3	2233	2	B95075	beta-galactosidase
36	266.5	8.2	2228	2	E97942	beta-galactosidase
37	232.5	7.2	900	2	T19689	hypothetical prote
38	168	5.2	785	2	H72228	hypothetical prote
39	157.5	4.9	431	2	T09048	probable mannan en
40	157.5	4.9	879	2	A55881	beta-mannosidase (
41	155	4.8	369	2	T04323	mannan endo-1,4-be
42	152.5	4.7	891	2	A82755	beta-mannosidase p
43	152.5	4.7	946	2	G71617	SERA antigen/papai
44	152	4.7	403	2	A84592	(1-4)-beta-mannan
45	146	4.5	827	2	AB2764	beta-mannosidase p

GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 20, 2006, 09:07:58 ; Search time 303 Seconds
                                              (without alignments)
                                   1825.608 Million cell updates/sec

Title: US-10-673-935-2
Perfect score: 3244
Sequence: 1 MESALYPIQNKYRFNTLMNG..........RDREPKDIAFTLKKRWQQLN 598

Scoring table: BLOSUM62
                   Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   UniProt_7.2:*
                   1: uniprot_sprot:*
                   2: uniprot_trembl:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                                SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	3244	100.0	598	2	Q9AHJ8_9LACO	Q9ahj8 lactobacill
2	1779	54.8	603	2	Q6W7J7_RUMGN	Q6w7j7 ruminococcu
3	1268	39.1	599	2	Q8VNV4_CLOPE	Q8vnv4 clostridium
4	1266	39.0	599	2	Q8XP19_CLOPE	Q8xp19 clostridium
5	1210.5	37.3	602	2	Q9AFA2_9STAP	Q9afa2 staphylococ
6	1207.5	37.2	603	1	BGLR_ECOLI	P05804 escherichia
7	1207.5	37.2	603	2	Q3Z1X0_SHISS	Q3z1x0 shigella so
8	1207.5	37.2	603	2	Q8FHA3_ECOL6	Q8fha3 escherichia
9	1205.5	37.2	603	2	Q93VY4_ARATH	Q93vy4 arabidopsis
10	1204.5	37.1	603	2	Q9AHJ4_ECOLI	Q9ahj4 escherichia
11	1196	36.9	601	2	Q4L323_STAHJ	Q4l323 staphylococ
12	1165.5	35.9	599	2	Q301D2_STRSU	Q301d2 streptococc
13	1162.5	35.8	598	2	Q3WAS3_9ACTO	Q3was3 frankia sp.
14	1156.5	35.7	593	2	Q6A5C6_PROAC	Q6a5c6 propionibac
15	1144.5	35.3	590	2	Q3WB58_9ACTO	Q3wb58 frankia sp.
16	1143	35.2	641	2	Q5MJX9_9PEZI	Q5mjx9 scopulariop
17	1138	35.1	599	2	Q3DGP9_STRAG	Q3dgp9 streptococc
18	1138	35.1	599	2	Q3DM94_STRAG	Q3dm94 streptococc
19	1136	35.0	599	2	Q8E6A6_STRA3	Q8e6a6 streptococc
20	1134	35.0	599	2	Q3D1W9_STRAG	Q3d1w9 streptococc

21	1132	34.9	599	2	Q3K207_STRA1	Q3k207	streptococc
22	1130	34.8	599	2	Q3D9K8_STRAG	Q3d9k8	streptococc
23	1130	34.8	599	2	Q3DSU4_STRAG	Q3dsu4	streptococc
24	1130	34.8	599	2	Q8E0N2_STRA5	Q8e0n2	streptococc
25	1116.5	34.4	567	2	Q7UCE6_SHIFL	Q7uce6	shigella fl
26	1114.5	34.4	567	2	Q83RC5_SHIFL	Q83rc5	shigella fl
27	1113	34.3	604	2	Q2U3J6_ASPOR	Q2u3j6	aspergillus
28	1108.5	34.2	644	2	Q5B269_EMENI	Q5b269	aspergillus
29	1102	34.0	594	2	Q2PBR7_9STRE	Q2pbr7	streptococc
30	1092.5	33.7	612	2	Q4I5B5_GIBZE	Q4i5b5	gibberella
31	1077.5	33.2	634	2	Q5MJY2_9EURO	Q5mjy2	penicillium
32	1075	33.1	621	2	Q5MJX7_9MICC	Q5mjx7	arthrobacte
33	1074	33.1	618	2	Q5MJX5_9MICC	Q5mjx5	arthrobacte
34	1065.5	32.8	634	2	Q5MJY0_9EURO	Q5mjy0	penicillium
35	1021.5	31.5	656	2	Q59DS6_DROME	Q59ds6	drosophila
36	1021.5	31.5	656	2	Q9V8R0_DROME	Q9v8r0	drosophila
37	1021.5	31.5	670	2	Q6NL66_DROME	Q6nl66	drosophila
38	1021.5	31.5	670	2	Q8MMB7_DROME	Q8mmb7	drosophila
39	1016	31.3	624	2	Q7PZE2_ANOGA	Q7pze2	anopheles g
40	977.5	30.1	627	2	Q60UV5_CAEBR	Q60uv5	caenorhabdi
41	973	30.0	627	2	Q4SLE9_TETNG	Q4sle9	tetraodon n
42	960	29.6	686	2	Q9V9T9_DROME	Q9v9t9	drosophila
43	958.5	29.5	628	2	Q95Q32_CAEEL	Q95q32	caenorhabdi
44	953	29.4	651	1	BGLR_HUMAN	P08236	homo sapien
45	953	29.4	651	2	Q549U0_HUMAN	Q549u0	homo sapien

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#10 **Related Articles for PubMed (Select 11229918)**		08:14:58	305
#8 Search #7 AND gasseri		08:13:44	5
#7 Search **"Glucuronidase"[MeSH]**		08:13:27	10597

Clear History

Jul 11 2006 06:31:05

Search Strategy for 10/673,935

    (FILE 'HOME' ENTERED AT 12:53:55 ON 13 JUL 2006)

    FILE 'REGISTRY' ENTERED AT 12:55:35 ON 13 JUL 2006
L1   1 S 9001-45-0

    FILE 'MEDLINE, AGRICOLA, CAPLUS, BIOSIS, EMBASE, WPIDS' ENTERED AT
    12:55:51 ON 13 JUL 2006
L2   58261 S L1 OR B-GLUCURONIDASE OR BETA-GLUCURONIDASE OR KETODASE OR ?G
L3   415 S L2 AND LACTOBACILLUS
L4   26 S L2 AND GASSERI
L5   10 DUP REM L4 (16 DUPLICATES REMOVED)

=>

IUBMB Enzyme Nomenclature

EC 3.2.1.31

Common name: β-glucuronidase

Reaction: a β-D-glucuronoside + H_2O = D-glucuronate + an alcohol

Other name(s): β-glucuronide glucuronohydrolase glucuronidase; exo-β-D-glucuronidase; ketodase

Systematic name: β-D-glucuronoside glucuronosohydrolase

Links to other databases: BRENDA, EXPASY, KEGG, ERGO, PDB, CAS registry number: 9001-45-0

References:

1. Diez, T. and Cabezas, J.A. Properties of two molecular forms of β-glucuronidase from the mollusc *Littorina littorea* L. *Eur. J. Biochem.* 93 (1978) 301-311.

2. Doyle, M.L., Katzman, P.A. and Doisy, E.A. Production and properties of bacterial β-glucuronidase. *J. Biol. Chem.* 217 (1955) 921-930.

3. Fishman, W.H. Beta-glucuronidase. *Adv. Enzymol. Relat. Subj. Biochem.* 16 (1955) 361-409.

4. Levvy, G.A. and Marsh, C.A. β-Glucuronidase, in Boyer, P.D., Lardy, H. and Myrbäck, K. (Eds.), *The Enzymes*, 2nd edn., vol. 4, Academic Press, New York, 1960, pp. 397-407.

5. Wakabayashi, M. and Fishman, W.H. The comparative ability of β-glucuronidase preparations (liver, *Escherichia coli, Helix pomatia,* and *Patella vulgata*) to hydrolyze certain steroid glucosiduronic acids. *J. Biol. Chem.* 236 (1961) 996-1001.

[EC 3.2.1.31 created 1961]

EAST Search History

Ref #	Hits	Search Query	DBs	Default Operator	Plurals	Time Stamp
L1	379	gasseri	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2006/07/13 12:53
L2	7	L1 same ($glucuronidase or "3.2.1. 31")	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2006/07/13 12:54
L3	294	lactobacillus and ($glucuronidase or "3.2.1.31")	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2006/07/13 12:54
L4	49	lactobacillus same ($glucuronidase or "3.2.1.31")	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2006/07/13 12:54
L5	23	lactobacillus and $glucuronidase.clm.	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2006/07/13 13:02
L6	10	l1 and (russell.in. or klaenhammer.in.)	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2006/07/13 13:03
L7	4	l6 and $glucuronidase	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2006/07/13 13:03
S1	379	gasseri	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2006/07/13 09:02
S2	29	S1 and (glucuronidase or "3.2.1.31")	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2006/07/13 09:03
S3	7	S1 same (glucuronidase or "3.2.1.31")	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2006/07/13 12:53

PATENT COOPERATION TREATY

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DECLARATION OF NON-ESTABLISHMENT OF INTERNATIONAL SEARCH REPORT

(PCT Article 17(2)(a), Rules 13ter and 39)

Applicant's or agent's file reference 5051.514.WO	IMPORTANT DECLARATION	Date of mailing *(day/month/year)*
International application No. PCT/US01/16667	International filing date *(day/month/year)* 22 MAY 2001	(Earliest) Priority Date *(day/month/year)* 22 MAY 2000

International Patent Classification (IPC) or both national classification and IPC
Please See Continuation Sheet.

Applicant
NORTH CAROLINA STATE UNIVERSITY

This International Searching Authority hereby declares, according to Article 17(2)(a), that no international search report will be established on the international application for the reasons indicated below.

1. ☐ The subject matter of the international application relates to:
   a. ☐ scientific theories.
   b. ☐ mathematical theories.
   c. ☐ plant varieties.
   d. ☐ animal varieties.
   e. ☐ essentially biological processes for the production of plants and animals, other than microbiological processes and the products of such processes.
   f. ☐ schemes, rules or methods of doing business.
   g. ☐ schemes, rules or methods of performing purely mental acts.
   h. ☐ schemes, rules or methods of playing games.
   i. ☐ methods for treatment of the human body by surgery or therapy.
   j. ☐ methods for treatment of the animal body by surgery or therapy.
   k. ☐ diagnostic methods practiced on the human or animal body.
   l. ☐ mere presentations of information.
   m. ☐ computer programs for which this International Searching Authority is not equipped to search prior art.

2. ☐ The failure of the following parts of the international application to comply with prescribed requirements prevents a meaningful search from being carried out:
   ☐ the description   ☐ the claims   ☐ the drawings

3. ☒ The failure of the nucleotide and/or amino acid sequence listing to comply with the standard provided for in Annex C of the Administrative Instructions prevents a meaningful search from being carried out.
   ☐ the written form has not been furnished or does not comply with the standard.
   ☒ the computer readable form has not been furnished or does not comply with the standard.

4. Further comments:
   Please See Continuation Sheet.

Name and mailing address of the ISA/US Commissioner of Patents and Trademarks Box PCT Washington, D.C. 20231	Authorized officer PADMA BASKAR
Facsimile No. (703) 305-3230	Telephone No. (703) 308-0196

Form PCT/ISA/203 (July 1998)*

The International Patent Classification (IPC) or National Classification and IPC are as listed below:

US.Cl : 536/23.1, 23.2, 23.6; 530/350, 387.1, 388.1; 435/69.1; 424/130.1
IPC (7): C07H 21/02, 21/04; C07K 1/00, 16/00; C12P 21/06; A61K 39/395

+. Further Comments (Continued):

The invention is directed to a polynucleotide encoding Betaglucoronidse , SEQ.ID.NO: 1. However, search could not be performed because of errors in the computer readable form. Please see attached error report.